



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/815,337

DATE: 09/29/2004
TIME: 13:05:45

Input Set : A:\Sequence listing.ST25.txt
Output Set: N:\CRF4\09292004\J815337.raw

3 <110> APPLICANT: Gurtu, V
5 <120> TITLE OF INVENTION: Renilla GFP MUTANTS WITH INCREASED FLUORESCENT INTENSITY
7 <130> FILE REFERENCE: 25436/2412
9 <140> CURRENT APPLICATION NUMBER: US 10/815,337

C--> 10 <141> CURRENT FILING DATE: 2004-04-01
12 <150> PRIOR APPLICATION NUMBER: 60/460,432
13 <151> PRIOR FILING DATE: 2003-04-04
15 <160> NUMBER OF SEQ ID NOS: 80
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 720
21 <212> TYPE: DNA
22 <213> ORGANISM: Renilla reniformis
24 <400> SEQUENCE: 1

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29	atccttgc	gcaaccagct	ggtgcagatc	cgcgtgacca	agggccccc	cctgccttc		180
31	gccttcgaca	tcctgagccc	cgcctccag	tacggcaacc	gcacccatc	caagtacccc		240
33	gaggacatca	gcgacttctt	catccagagc	ttccccgcgg	gcttcgtgta	cgagcgcacc		300
35	ctgcgttacg	aggacggcg	cctggggag	atccgcagcg	acatcaacct	gatcgaggag		360
37	atgttcgtgt	accgcgtgga	gtacaagg	cgcaacttcc	ccaacgcagg	ccccgtgatg		420
39	aagaagacca	tcacccgcct	gcagccgc	tgcggatgg	tgtacatgaa	cgacggcg		480
41	ctggggcc	aggtgatcct	ggtgtaccgc	ctgaacagcg	gcaagttcta	cagctgccac		540
43	atgcgcaccc	tgtatgaa	caagggcg	gtgaaaggact	tcccccagta	ccacttcatc		600
45	cagcaccgc	ttggagaagac	ctacgtggag	gacggcggt	tcgtggagca	gcacgagacc		660
47	gccatcgccc	agctgaccag	cctggcaag	cccctggca	gcctgcacga	gtgggtgtaa		720

50 <210> SEQ ID NO: 2

51 <211> LENGTH: 239

52 <212> TYPE: PRT

53 <213> ORGANISM: Renilla reniformis

55 <400> SEQUENCE: 2

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58 1	5	10	15
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61 Ser Phe Lys Val Asn Leu Glu Gly Val Val Asn Asn His Val Phe Thr

62 20	25	30
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65 Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val

66 35	40	45
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69 Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile

70 50	55	60
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73 Leu Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro

74 65	70	75	80
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77 Glu Asp Ile Ser Asp Phe Phe Ile Gln Ser Phe Pro Ala Gly Phe Val

78 85	90	95
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81 Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg
82 100 105 110
85 Ser Asp Ile Asn Leu Ile Glu Glu Met Phe Val Tyr Arg Val Glu Tyr
86 115 120 125
89 Lys Gly Arg Asn Phe Pro Asn Asp Gly Pro Val Met Lys Lys Thr Ile
90 130 135 140
93 Thr Gly Leu Gln Pro Ser Phe Glu Val Val Tyr Met Asn Asp Gly Val
94 145 150 155 160
97 Leu Val Gly Gln Val Ile Leu Val Tyr Arg Leu Asn Ser Gly Lys Phe
98 165 170 175
101 Tyr Ser Cys His Met Arg Thr Leu Met Lys Ser Lys Gly Val Val Lys
102 180 185 190
105 Asp Phe Pro Glu Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr
106 195 200 205
109 Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln
110 210 215 220
113 Leu Thr Ser Leu Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
114 225 230 235
117 <210> SEQ ID NO: 3
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119 <212> TYPE: DNA
120 <213> ORGANISM: Renilla reniformis
122 <400> SEQUENCE: 3
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125 aacctggagg gcgtggtaa caaccacgt ttcaccatgg agggctgcgg caaggcaac 120
127 atccctgttag gcaaccagct ggtcagatc cgcgtgacca agggcgcccc cctgccttc 180
129 gccttcgaca tcctgagccc cgccttccag tacggcaacc gcaccttcac caagtacccc 240
131 gaggacatca gcgacttctt catccagagc ttcccgccc gcttcgtgta cgagcgcacc 300
133 ctgcgctacg aggacggcgg cctggtgag atcccgagcg acatcaacct gatcgaggag 360
135 atgttcgtgt accgcgtgga gtacaaggcc cgcaacctcc ccaacgcagg ccccgatg 420
137 aagaagacca tcacccgcct gcagcccagc ttcgaggtgg tgtacatgaa cgacggcgtg 480
139 ctgggggcc aggtgatcct ggttacccg ctgaacagcg gcaagttcta cagctgccac 540
141 atgcgcaccc tcatgaagag caagggcgtg gtgaaggact tcccgagata ccacttcac 600
143 cagcaccgccc tggagaagac ctacgtggag gacggcggt tcgtggagca gcacgagacc 660
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149 <211> LENGTH: 239
150 <212> TYPE: PRT
151 <213> ORGANISM: Renilla reniformis
153 <400> SEQUENCE: 4
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159 Ser Phe Lys Val Asn Leu Glu Gly Val Val Asn Asn His Val Phe Thr
160 20 25 30
163 Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Leu Gly Asn Gln Leu Val
164 35 40 45
167 Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile
168 50 55 60
171 Leu Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro

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172	65	70	75	80												
175	Glu	Asp	Ile	Ser	Asp	Phe	Phe	Ile	Gln	Ser	Phe	Pro	Ala	Gly	Phe	Val
176					85				90						95	
179	Tyr	Glu	Arg	Thr	Leu	Arg	Tyr	Glu	Asp	Gly	Gly	Leu	Val	Glu	Ile	Arg
180					100				105						110	
183	Ser	Asp	Ile	Asn	Leu	Ile	Glu	Glu	Met	Phe	Val	Tyr	Arg	Val	Glu	Tyr
184					115				120						125	
187	Lys	Gly	Arg	Asn	Phe	Pro	Asn	Asp	Gly	Pro	Val	Met	Lys	Lys	Thr	Ile
188					130				135						140	
191	Thr	Gly	Leu	Gln	Pro	Ser	Phe	Glu	Val	Val	Tyr	Met	Asn	Asp	Gly	Val
192	145				150				155						160	
195	Leu	Val	Gly	Gln	Val	Ile	Leu	Val	Tyr	Arg	Leu	Asn	Ser	Gly	Lys	Phe
196					165				170						175	
199	Tyr	Ser	Cys	His	Met	Arg	Thr	Leu	Met	Lys	Ser	Lys	Gly	Val	Val	Lys
200					180				185						190	
203	Asp	Phe	Pro	Glu	Tyr	His	Phe	Ile	Gln	His	Arg	Leu	Glu	Lys	Thr	Tyr
204					195				200						205	
207	Val	Glu	Asp	Gly	Gly	Phe	Val	Glu	Gln	His	Glu	Thr	Ala	Ile	Ala	Gln
208					210				215						220	
211	Leu	Thr	Ser	Leu	Gly	Lys	Pro	Leu	Gly	Ser	Leu	His	Glu	Trp	Val	
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223	aacctggagg	gcgtgtgaa	caaccacgtg	ttcaccatgg	agggctgcgg	caaggcaac									120	
225	atcctgttcg	gcaaccagct	ggtgcagatc	cgcgtacca	agggcgcccc	cctgccttc									180	
227	gccttcgaca	tcctgagccc	cgccttcag	tacggcaacc	gcaccttcac	caagtacccc									240	
229	gaggacatca	gcgacttctt	catccagagc	ttccccgccc	gttcgtgtt	cgagcgcacc									300	
231	ctgcgtctacg	aggacggcgg	cctggtggag	atccgtcg	acatcaaccc	gatcgagggg									360	
233	atgttcgtgt	accgcgtgga	gtacaaggggc	cgcaacttcc	ccaacgacgg	ccccgtgatg									420	
235	aagaagacca	tcacccgcct	gcagcccagc	ttcgaggtgg	tgtacatgaa	cgacggcgtg									480	
237	ctgggtggcc	aggtgatcct	ggtgtaccgc	ctgaacagcg	gcaagttcta	cagctgccac									540	
239	atgcgcaccc	tgtatgaaagag	caagggcgtg	gtgaaggact	tcccccgtgt	ccacttcatc									600	
241	cagcaccgc	tggagaagac	ctacgtggag	gacggcgct	tctgttagagca	gcacgagacc									660	
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257	Ser	Phe	Lys	Val	Asn	Leu	Glu	Gly	Val	Val	Asn	Asn	His	Val	Phe	Thr
258					20				25						30	
261	Met	Glu	Gly	Cys	Gly	Lys	Asn	Ile	Leu	Phe	Gly	Asn	Gln	Leu	Val	
262					35				40						45	

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265 Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile
 266 50 55 60
 269 Leu Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro
 270 65 70 75 80
 273 Glu Asp Ile Ser Asp Phe Phe Ile Gln Ser Phe Pro Ala Gly Phe Val
 274 85 90 95
 277 Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg
 278 100 105 110
 281 Ser Asp Ile Asn Leu Ile Glu Gly Met Phe Val Tyr Arg Val Glu Tyr
 282 115 120 125
 285 Lys Gly Arg Asn Phe Pro Asn Asp Gly Pro Val Met Lys Lys Thr Ile
 286 130 135 140
 289 Thr Gly Leu Gln Pro Ser Phe Glu Val Val Tyr Met Asn Asp Gly Val
 290 145 150 155 160
 293 Leu Val Gly Gln Val Ile Leu Val Tyr Arg Leu Asn Ser Gly Lys Phe
 294 165 170 175
 297 Tyr Ser Cys His Met Arg Thr Leu Met Lys Ser Lys Gly Val Val Lys
 298 180 185 190
 301 Asp Phe Pro Glu Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr
 302 195 200 205
 305 Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln
 306 210 215 220
 309 Leu Thr Ser Leu Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
 310 225 230 235
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 315 <212> TYPE: DNA
 316 <213> ORGANISM: Renilla reniformis
 318 <400> SEQUENCE: 7
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 323 atccctgttcg gcaaccagct ggtcagatc cgcgtgacca agggcgcccc cctgccttc 180
 325 gccttcgaca tcctgagccc cgccctccag tacggcaacc gcacccatc caagtacccc 240
 327 gaggacatca gctacttcatccagagc ttcccccgcg gttcgtgtt ctagcgcacc 300
 329 atgcgtacg aggacggcg cctgggtggat atccgcagcg acatcaacct gatcgaggag 360
 331 atgttcgtgtt accgcgtgga gtacaaggcg cgcaacttcc ccaacgacgg cccctgtatg 420
 333 aagaagacca tcaccggcct gcagcccgat ttcgaggtgg tttatcatgaa cgacggcg 480
 335 ctgggtggcc aggtgtatcct ggtgtaccgc ctgaacagcg gcaagttcta cagctgccac 540
 337 atgcgcaccc tggatggatggat caagggcgat gtggaggact tcccccgttccacttcatc 600
 339 cagcaccgccc tggatggatggat caagggcgat gtggaggact tcccccgttccacttcatc 660
 341 gccatcgccc agctgaccag cctggcaag cccctggcaag gcctgcacga gtgggtgtaa 720
 344 <210> SEQ ID NO: 8
 345 <211> LENGTH: 239
 346 <212> TYPE: PRT
 347 <213> ORGANISM: Renilla reniformis
 349 <400> SEQUENCE: 8
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 352 1 5 10 15
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356	20	25	30													
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360									35		40				45	
363	Gln	Ile	Arg	Val	Thr	Lys	Gly	Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile
364									50		55			60		
367	Leu	Ser	Pro	Ala	Phe	Gln	Tyr	Gly	Asn	Arg	Thr	Phe	Thr	Lys	Tyr	Pro
368									65		70			75		80
371	Glu	Asp	Ile	Ser	Asp	Phe	Phe	Ile	Gln	Ser	Phe	Pro	Ala	Gly	Phe	Val
372									85		90			95		
375	Tyr	Glu	Arg	Thr	Met	Arg	Tyr	Glu	Asp	Gly	Gly	Leu	Val	Glu	Ile	Arg
376									100		105			110		
379	Ser	Asp	Ile	Asn	Leu	Ile	Glu	Glu	Met	Phe	Val	Tyr	Arg	Val	Glu	Tyr
380									115		120			125		
383	Lys	Gly	Arg	Asn	Phe	Pro	Asn	Asp	Gly	Pro	Val	Met	Lys	Lys	Thr	Ile
384									130		135			140		
387	Thr	Gly	Leu	Gln	Pro	Ser	Phe	Glu	Val	Val	Tyr	Met	Asn	Asp	Gly	Val
388									145		150			155		160
391	Leu	Val	Gly	Gln	Val	Ile	Leu	Val	Tyr	Arg	Leu	Asn	Ser	Gly	Lys	Phe
392									165		170			175		
395	Tyr	Ser	Cys	His	Met	Arg	Thr	Leu	Met	Lys	Ser	Lys	Gly	Val	Val	Lys
396									180		185			190		
399	Asp	Phe	Pro	Glu	Tyr	His	Phe	Ile	Gln	His	Arg	Leu	Glu	Lys	Thr	Tyr
400									195		200			205		
403	Val	Glu	Asp	Gly	Gly	Phe	Val	Glu	Gln	His	Glu	Thr	Ala	Ile	Ala	Gln
404									210		215			220		
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421	atccgtccg	gcaaccagct	ggtgcagatc	cgcgtgacca	agggcgcggcc	cctgccttc									180	
423	gccttcgaca	tcctgagcccc	cgccttccag	tacggcaacc	gcacccatcac	caagtacccc									240	
425	gaggacatca	gcgacttctt	catccagagc	ttcccccggcc	gcttcgtgt	cgagcgcacc									300	
427	ctgcgcgtacg	aggacggcg	cctgggtggag	atccgcagcg	acatcaacct	gatcgaggag									360	
429	atgttcgtgt	accgcgtgga	gtacaagggc	cgcaacttcc	ccaaacgacgg	ccccgtgtat									420	
431	aagaagacca	tcaccggcc	gcagcccagc	ttcgagggtgg	tgtacatgaa	cgacggcggt									480	
433	ctggggggcc	aggtgatcc	ggtgatccgc	ctgaacagcg	gcaaggctcta	cagctgcac									540	
435	atgcgcaccc	tgtatgaaagag	caagggcggt	gtgaaggact	tcccccagta	ccacttcatc									600	
437	cagcaccgc	tggagaagac	ctacgtggag	gacggcggt	tcgtggagca	gcacgagacc									660	
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442	<210> SEQ ID NO: 10															
443	<211> LENGTH: 239															
444	<212> TYPE: PRT															
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nvalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:63,64,65,66,67,68,70,71,72,73,74,75,76,77,78,80

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date